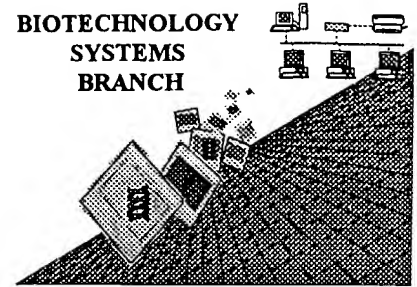


A. Gupta

# RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



PH#6

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/423,545A  
Art Unit / Team No. : 1653  
Date Processed by STIC: 3/29/2000

RECEIVED  
FEB 12 2000  
TC 1600 MAIL ROOM

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

**1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**

**2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**MARK SPENCER 703-308-4212**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/423,545A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2      Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3      Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4      Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5      Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6      Variable Length      Sequence(s)      contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7      PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)                     . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence.
- 8      Skipped Sequences      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9      Skipped Sequences      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                                 <400> sequence id number  
                                 000
- 10    Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11      Use of <213>Organism      Sequence(s)              are missing this mandatory field or its response.  
(NEW RULES)
- 12      Use of <220>Feature      Sequence(s)      are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13      PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RECEIVED  
APR 12 2000  
TC 100 MAIL ROOM

PAGE: 1

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/423,545A

DATE: 03/29/2000  
TIME: 15:44:28

Input Set: I423545A.RAW

This Raw Listing contains the General  
Information Section and those Sequences  
containing ERRORS.

1 <110> Kenji SHIBATA  
2 Motoo YAMASAKI  
3 Tetsuo YOSHIDA  
4 Tamio MIZUKAMI  
5 Akeo SHINKAI  
6 Hideharu ANAZAWA  
7 <120> Peptides having a cyclic structure and restoring the  
8 activities of P53 protein to mutant P53 protein  
9 <130> 1061  
10 <140> US/09/423,545A  
11 <141> 1999-11-12  
12 <150> JP97/126113  
13 <151> 1997-05-15  
14 <160> 32

Does Not Comply  
Corrected Diskette Needed

## ERRORED SEQUENCES FOLLOW

(See item 1 on  
Erra Summary Sheet)

E--> 15 <210> 8  
16 <211> 32  
17 <212> DNA  
18 <213> Artificial Sequence  
19 <220>  
20 <223> Other nucleic acid Synthetic DNA  
21 <400> 8  
E--> 22 CTAGACAGCC AGACTGCCTT CCGGGTCACT GC  
23 32

per new sequence rules,  
bases must be in

lower-case  
letters

format error

→ 32

E--> 24 <210> 9  
25 <211> 32  
26 <212> DNA  
27 <213> Artificial Sequence  
28 <220>  
29 <223> Other nucleic acid Synthetic DNA  
30 <400> 9  
E--> 31 CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT  
32 32

→ 32

E--> 33 <210> 10  
34 <211> 26  
35 <212> DNA  
36 <213> Artificial Sequence  
37 <220>

PAGE: 2

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/423,545A

DATE: 03/29/2000  
TIME: 15:44:28

Input Set: I423545A.RAW

38 <223> Other nucleic acid Synthetic DNA  
39 <400> 10  
E--> 40 TCGAGAGACA TGCCTAGACA TGCCTG  
41 26

42 <210> 11  
E--> 43 <211> 26  
44 <212> DNA  
45 <213> Artificial Sequence  
46 <220>  
47 <223> Other nucleic acid Synthetic DNA  
48 <400> 11  
E--> 49 TCGACAGGCA TGTCTAGGCA TGTCTC  
50 26

51 <210> 12  
E--> 52 <211> 22  
53 <212> DNA  
54 <213> Artificial Sequence  
55 <220>  
56 <223> Other nucleic acid Synthetic DNA  
57 <400> 12  
E--> 58 TCGAGCCCGG GGGTACCGCA TG  
59 22

60 <210> 13  
E--> 61 <211> 14  
62 <212> DNA  
63 <213> Artificial Sequence  
64 <220>  
65 <223> Other nucleic acid Synthetic DNA  
66 <400> 13  
E--> 67 CGGTACCCCC GGGC  
68 14

69 <210> 14  
E--> 70 <211> 32  
71 <212> DNA  
72 <213> Artificial Sequence  
73 <220>  
74 <223> Other nucleic acid Synthetic DNA  
75 <400> 14  
E--> 76 TCGAGGGACT TGCCTGGACT TGCCTGTCTGA CG  
77 32

78 <210> 15  
E--> 79 <211> 32  
80 <212> DNA  
81 <213> Artificial Sequence  
82 <220>

*same  
format  
env*

↓

PAGE: 3

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/423,545A

DATE: 03/29/2000

TIME: 15:44:28

Input Set: I423545A.RAW

83 <223> Other nucleic acid Synthetic DNA  
84 <400> 15  
E--> 85 GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC  
86 32

*same*

87 <210> 24  
E--> 88 <211> 16 15 slow  
89 <212> PRT  
90 <213> Artificial Sequence  
91 <220>  
92 <221> BINDING  
93 <222> (7)..(13)  
94 <223> BINDING type is -CONH2-.  
95 <220>  
96 <221> SITE  
97 <222> (15)  
98 <223> Xaa represents L-Leucine amide.  
99 <220>  
100 <223> Synthetic peptide  
101 <400> 24  
W--> 102 Leu Lys Ser Lys Lys Gly Asp Ser Thr Ser Arg His Lys Lys Xaa  
103 1 5 10 15

*move amino acid nos. directly under  
amino acids*

*↓ FYI*

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I423545A.RAW

Line	? Error/Warning	Original Text
16	E Input 32, Calc# Bases 0 differ	<211> 32
22	E Wrong Amino Acid Designator	CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
22	E Wrong Amino Acid Designator	CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
22	E Wrong Amino Acid Designator	CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
22	E Wrong Amino Acid Designator	CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
25	E Input 32, Calc# Bases 0 differ	<211> 32
31	E Wrong Amino Acid Designator	CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
31	E Wrong Amino Acid Designator	CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
31	E Wrong Amino Acid Designator	CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
31	E Wrong Amino Acid Designator	CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
34	E Input 26, Calc# Bases 0 differ	<211> 26
40	E Wrong Amino Acid Designator	TCGAGAGACA TGCCTAGACA TGCCTG
40	E Wrong Amino Acid Designator	TCGAGAGACA TGCCTAGACA TGCCTG
40	E Wrong Amino Acid Designator	TCGAGAGACA TGCCTAGACA TGCCTG
43	E Input 26, Calc# Bases 0 differ	<211> 26
49	E Wrong Amino Acid Designator	TCGACAGGCA TGTCTAGGCA TGTCTC
49	E Wrong Amino Acid Designator	TCGACAGGCA TGTCTAGGCA TGTCTC
49	E Wrong Amino Acid Designator	TCGACAGGCA TGTCTAGGCA TGTCTC
52	E Input 22, Calc# Bases 0 differ	<211> 22
58	E Wrong Amino Acid Designator	TCGAGCCCCG GGGTACCGCA TG
58	E Wrong Amino Acid Designator	TCGAGCCCCG GGGTACCGCA TG
58	E Wrong Amino Acid Designator	TCGAGCCCCG GGGTACCGCA TG
61	E Input 14, Calc# Bases 0 differ	<211> 14
67	E Wrong Amino Acid Designator	CGGTACCCCC GGGC
67	E Wrong Amino Acid Designator	CGGTACCCCC GGGC
70	E Input 32, Calc# Bases 0 differ	<211> 32
76	E Wrong Amino Acid Designator	TCGAGGGGACT TGCCTGGACT TGCCTGTCGA CG
76	E Wrong Amino Acid Designator	TCGAGGGGACT TGCCTGGACT TGCCTGTCGA CG
76	E Wrong Amino Acid Designator	TCGAGGGGACT TGCCTGGACT TGCCTGTCGA CG
76	E Wrong Amino Acid Designator	TCGAGGGGACT TGCCTGGACT TGCCTGTCGA CG
79	E Input 32, Calc# Bases 0 differ	<211> 32
85	E Wrong Amino Acid Designator	GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
85	E Wrong Amino Acid Designator	GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
85	E Wrong Amino Acid Designator	GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
85	E Wrong Amino Acid Designator	GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
88	E Input 16, Calc Seq.Length 15 differ	<211> 16
102	W "N" or "Xaa" used: Feature required	Leu Lys Ser Lys Lys Gly Asp Ser Thr Ser A